

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2001, 11:28:20 ; Search time 13.33 Seconds
(without alignments)
97.147 Million cell updates/sec

Title: US-09-497-997B-1

Perfect score: 98
Sequence: 1 TRQYKRAMDYWGQGT 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	66.3	122	2 E27888	Ig heavy chain V r
2	64.5	65.8	139	2 PS0024	Ig heavy chain pre
3	63	64.3	120	2 S03484	Ig heavy chain V-D
4	62	63.3	119	2 S09955	Ig heavy chain V-D
5	62	63.3	138	2 E32513	Ig heavy chain pre
6	62	62.2	99	2 S26326	Ig heavy chain V r
7	61	62.2	120	2 E45722	anti-glycoprotein
8	60.5	61.7	122	2 S20642	Ig heavy chain V r
9	60	61.2	104	2 S28466	Ig heavy chain V r
10	60	61.2	117	2 S38563	Ig heavy chain V r
11	59.5	60.7	122	2 S20643	Ig heavy chain V r
12	59	60.2	101	2 D24672	Ig heavy chain V r
13	59	60.2	107	2 S26320	Ig heavy chain V r
14	59	60.2	109	2 S26318	Ig heavy chain V r
15	59	60.2	111	2 S26324	Ig heavy chain V r
16	59	60.2	112	2 B27563	Ig heavy chain V r
17	59	60.2	118	2 S20641	Ig heavy chain V r
18	59	60.2	136	2 S04576	Ig heavy chain pre
19	59	60.2	139	2 A27609	Ig heavy chain pre
20	58.5	59.7	123	2 S20646	Ig heavy chain V r
21	58	59.2	119	2 F27888	Ig heavy chain V r
22	57.5	58.7	113	2 S26468	Ig heavy chain V r
23	57.5	58.7	120	2 S41394	Ig heavy chain V r
24	57	58.2	30	2 PL0092	Ig heavy chain V r
25	57	58.2	110	2 S26323	Ig heavy chain V r
26	57	58.2	111	2 PH1643	Ig heavy chain V r
27	57	58.2	114	2 PL0256	Ig heavy chain V r
28	57	58.2	125	2 PH0100	Ig heavy chain V r
29	57	58.2	149	2 S30752	Ig heavy chain pre

30 57 58.2 246 2 S38950 Ig gamma chain - m
31 57 58.2 446 2 S40295 Ig gamma-2a chain
32 56.5 57.7 117 2 PL0237 Ig heavy chain V r
33 56.5 57.7 117 2 PL0234 Ig heavy chain V r
34 56 57.1 119 2 D30540 Ig heavy chain V r
35 56 57.1 120 2 S55536 Ig heavy chain V r
36 56 57.1 120 2 S55539 Ig heavy chain V r
37 56 57.1 120 2 S55537 Ig heavy chain V r
38 56 57.1 120 2 PD0008 Ig heavy chain V r
39 56 57.1 122 2 S24287 Ig heavy chain V r
40 56 57.1 123 2 S32186 Ig heavy chain V r
41 56 57.1 136 1 GIMS21 Ig heavy chain pre
42 56 57.1 151 2 PL0011 Ig heavy chain pre
43 56 57.1 254 2 B31790 Ig heavy chain V r
44 55.5 56.6 126 2 S31930 Ig gamma chain pre
45 55 56.1 10 2 F33932 Ig mu chain J regi

ALIGNMENTS

RESULT 1

E27888
Ig heavy chain V region (H35-C6) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: E27888
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to
A:Reference number: A91043; MUID:86300658
A:Accession: E27888
A:Molecule type: DNA
A:Residues: 1-122 <CAT>
A:Experimental source: strain Balb/c
A:Note: This sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 65; DB 2; Length 122;
Best Local Similarity 61.9%; Pred. No. 0.0057;
Matches 13; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

Qy 1 TRQ----KYNKRAMDYWGQGT 17
||| :|: |||||
Db 97 TRQEGYRYDDYAMDYWGQGT 117

RESULT 2

PS0024
Ig heavy chain precursor V region (6A4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996
C:Accession: PS0024
R:Marget, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.
Gene 74, 335-345, 1988
A:Title: Cloning and characterization of cDNAs coding for the heavy and light chains
A:Reference number: PS0023; MUID:89233725
A:Accession: PS0024
A:Molecule type: mRNA
A:Residues: 1-139 <MAR>
A:Experimental source: strain BALB/c
C:Comment: This chain is obtained from an IgG2a monoclonal antibody against Pseudomon
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin; pyroglytamic acid
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-139/Domain: Ig heavy chain V region #status predicted <IGV>
F:34-117/Domain: immunoglobulin homology <IMM>
F:20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predic

Query Match 65.8%; Score 64.5; DB 2; Length 139;
 Best Local Similarity 72.2%; Pred. No. 0.0076;
 Matches 13; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 TROKYN-KRAMDYWGQGT 17
 ||| : |||||
 Db 116 TRSYNYEGAMDYWGQGT 133

RESULT 3
 S03484
 Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 A:Variety: strain BALB/c
 C:Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
 C:Accession: S03484; S07453
 R:Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.
 EMPBL J. 2, 867-872, 1983
 A:Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT
 hy-variable regions.
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>
 A:Reference number: S03471; MUID:84057768
 A:Accession: S03484
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 10-120 <ROCI>
 A:Cross-references: EMBL:X07144
 A:Note: this sequence was determined from the differentiated gene
 R:Rocca-Serra, J.; Mazie, J.C.; Moirier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere
 J. Immunol. 129, 2554-2558, 1982
 A:Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
 A:Reference number: S07453; MUID:83058021
 A:Accession: S07453
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-43 <ROC2>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 64.3%; Score 63; DB 2; Length 120;
 Best Local Similarity 64.7%; Pred. No. 0.011;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 TROKYN-KRAMDYWGQGT 17
 ||| : |||||
 Db 97 TRGWFRDAMDYWGQGT 113

RESULT 4
 S09955
 Ig heavy chain V-D-J region (103-7E) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
 C:Accession: S09955
 R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
 Eur. J. Immunol. 20, 771-777, 1990
 A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
 A:Reference number: S09955; MUID:90269328
 A:Accession: S09955
 A:Molecule type: mRNA
 A:Residues: 1-119 <REI>
 A:Cross-references: EMBL:X51843; NID:g55242; PIDN:CAA36136.1; PID:g930211
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 63.3%; Score 62; DB 2; Length 119;
 Best Local Similarity 70.6%; Pred. No. 0.016;
 Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TROKYN-KRAMDYWGQGT 17

Db 97 TRQSGTWDAMDYWGQGT 113
 ||| : |||||

RESULT 5
 E32513
 Ig heavy chain precursor V region (MRL22) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 23-Jul-1999
 C:Accession: E32513
 R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.
 J. Clin. Invest. 82, 852-860, 1988
 A:Title: Immunoglobulin kappa light chain variable region gene complex organization a
 A:Reference number: A94689; MUID:88331394
 A:Accession: E32513
 A:Molecule type: DNA
 A:Residues: 1-138 <KOF>
 A:Cross-references: GB:M20835; NID:g196945; PIDN:AAA38847.1; PID:g196946
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 63.3%; Score 62; DB 2; Length 138;
 Best Local Similarity 68.8%; Pred. No. 0.018;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ROKYNKRAMDYWGQGT 17
 ||| : |||||
 Db 117 RLRYRYAMDYWGQGT 132

RESULT 6
 S26326
 Ig heavy chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998
 C:Accession: S26326
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protei
 A:Reference number: S26309; MUID:91341421
 A:Accession: S26326
 A:Molecule type: mRNA
 A:Residues: 1-99 <STA>
 A:Cross-references: EMBL:X59174
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 62.2%; Score 61; DB 2; Length 99;
 Best Local Similarity 68.8%; Pred. No. 0.019;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ROKYNKRAMDYWGQGT 17
 ||| : |||||
 Db 78 REGYVYAMDYWGQGT 93

RESULT 7
 E45722
 anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 5) - mouse (anti-
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: E45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
 J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
 A:Reference number: A45722; MUID:93100833
 A:Accession: E45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-120 <SIM>

A:Note: sequence extracted from NCBI backbone (NCBIP:120593)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 62.2%; Score 61; DB 2; Length 120;
Best Local Similarity 58.8%; Pred. No. 0.023;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 TRQYKNKRAMDYWGQGT 17
II::: :|||||
Db 98 TRRGFRDYSMDYWGQGT 114

RESULT 8

Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S20642
R:Lozman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice re
A:Reference number: S20639
A:Accession: S20642
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-122 <LOS>
A:Cross-references: EMBL:X64997; NID:g52604; PIDN:CAA46130.1; PID:g52605
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 61.7%; Score 60.5; DB 2; Length 122;
Best Local Similarity 66.7%; Pred. No. 0.028;
Matches 12; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 TRQYKNKRAMDYWGQGT 17
II::: :|||||
Db 99 TRKAASRRGAMDYWGQGT 116

RESULT 9

Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26466
R:Valer, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26466
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-104 <KAV>
A:Cross-references: EMBL:X59116; NID:g51933; PIDN:CAA41842.1; PID:g51934
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:3-86/Domain: immunoglobulin homology <IMM>

Query Match 61.2%; Score 60; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RAMDYWGQGT 17
II|||||
Db 90 RAMDYWGQGT 99

RESULT 10

S38563
Ig heavy chain V region (AWS1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38563
R:Monestier, M.; Lozman, L.J.; Novick, K.E.; Aris, J.P.
submitted to the EMBL Data Library, September 1993
A:Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2

A:Reference number: S38559
A:Accession: S38563
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-117 <MON>
A:Cross-references: EMBL:X75099; NID:g414151; PIDN:CAA52990.1; PID:g414152
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 61.2%; Score 60; DB 2; Length 117;
Best Local Similarity 68.8%; Pred. No. 0.032;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 RQYKNKRAMDYWGQGT 17
I:| | | | |
Db 97 RDGYDYAMDYWGQGT 112

RESULT 11

S20643
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S20643
R:Lozman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice re
A:Reference number: S20639
A:Accession: S20643
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-122 <LOS>
A:Cross-references: EMBL:X64998; NID:g52606; PIDN:CAA46131.1; PID:g52607
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 60.7%; Score 59.5; DB 2; Length 122;
Best Local Similarity 63.2%; Pred. No. 0.04;
Matches 12; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 2 RQYKNKRAMDYWGQGT 17
I:| | | | |
Db 99 REYDRLRRGHAMDYWGQGT 117

RESULT 12

D24672
Ig heavy chain V region (VGAM3-8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
C:Accession: D24672
R:Winter, E.; Radbruch, A.; Krawinkel, U.
EMBO J. 4, 2861-2867, 1985
A:Reference number: A91022; MUID:86055722
A:Accession: D24672
A:Molecule type: DNA
A:Residues: 1-101 <WIN>
A:Cross-references: GB:X03301; NID:g51757; PIDN:CRAA27040.1; PID:g773215
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 60.2%; Score 59; DB 2; Length 101;
Best Local Similarity 76.9%; Pred. No. 0.04;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 YNKRMDYWGQGT 17
I: |||||
Db 83 YDYAMDYWGQGT 95

RESULT 13

S26320

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C:Accession: S26320

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein e

A:Reference number: S26309; MUID:91341421

A:Accession: S26320

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-107 <STA>

A:Cross-references: EMBL:X59206

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;3-86/Domain: immunoglobulin homology <IMM>

Query Match 60.2%; Score 59; DB 2; Length 107;
Best Local Similarity 76.9%; Pred. No. 0.042;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 YNKRMDYWGQGT 17
I: |||||
Db 90 YDYAMDYWGQGT 102

RESULT 14

S26318

Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000

C:Accession: S26318

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein e

A:Reference number: S26309; MUID:91341421

A:Accession: S26318

A:Molecule type: mRNA

A:Residues: 1-109 <STA>

A:Cross-references: EMBL:X59200

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;3-86/Domain: immunoglobulin homology <IMM>

Query Match 60.2%; Score 59; DB 2; Length 109;
Best Local Similarity 76.9%; Pred. No. 0.043;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 YNKRMDYWGQGT 17
I: |||||
Db 91 YFYAMDYWGQGT 103

RESULT 15

S26324

Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000

C:Accession: S26324
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protei
A:Reference number: S26309; MUID:91341421
A:Accession: S26324
A:Molecule type: mRNA
A:Residues: 1-111 <STA>
A:Cross-references: EMBL:X59178
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;7-88/Domain: immunoglobulin homology <IMM>

Query Match 60.2%; Score 59; DB 2; Length 111;
Best Local Similarity 83.3%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 NKRMDYWGQGT 17
I: |||||
Db 94 NYEAMDYWGQGT 105

Search completed: June 27, 2001, 11:28:54
Job time: 34 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2001, 11:28:20 ; Search time 19.1 seconds
(without alignments)
53.959 Million cell updates/sec

Title: US-09-497-997B-1

Perfect score: 98

Sequence: 1 TRQYKRAMDYWGQGT 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_0601.*
- 1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
 - 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
 - 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
 - 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
 - 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
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 - 7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
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 - 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
 - 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98	100	0	17	20 AAW99559
2	88	89.8	17	20	AAW99561
3	83.5	85.2	18	20	AAW99562
4	64.5	65.8	159	10	AAW93079
5	64	65.3	140	18	AAW21841
6	62	63.3	119	16	AAW24940
7	62	63.3	119	18	AAW01578
8	62	63.3	133	16	AAW74960
9	62	63.3	135	16	AAW74961
10	62	63.3	143	21	AAW43867
11	62	63.3	144	21	AAW43857

12	62	63.3	436	21	AAW91026
13	61	62.2	119	13	AAW25730
14	61	62.2	119	22	AAW69679
15	61	62.2	119	22	AAW69680
16	61	62.2	119	22	AAW69692
17	61	62.2	138	17	AAW03722
18	61	62.2	138	22	AAW69688
19	61	62.2	139	13	AAW27053
20	61	62.2	139	14	AAW30480
21	61	62.2	141	21	AAW43869
22	61	62.2	142	21	AAW43868
23	61	62.2	184	17	AAW03726
24	60	61.2	12	20	AAW99560
25	60	61.2	118	16	AAW79865
26	60	61.2	119	21	AAW92156
27	60	61.2	141	21	AAW43859
28	60	61.2	145	21	AAW43856
29	60	61.2	147	21	AAW43860
30	59	60.2	118	15	AAW50323
31	59	60.2	118	16	AAW79242
32	59	60.2	122	15	AAW50311
33	59	60.2	122	15	AAW50312
34	59	60.2	122	15	AAW50315
35	59	60.2	124	18	AAW01594
36	59	60.2	240	9	AAW80153
37	58	59.2	115	18	AAW04595
38	58	59.2	116	16	AAW64224
39	58	59.2	123	16	AAW81323
40	58	59.2	123	16	AAW81330
41	58	59.2	123	18	AAW07438
42	58	59.2	140	16	AAW81327
43	58	59.2	140	18	AAW22410
44	58	59.2	142	16	AAW81333
45	58	59.2	142	18	AAW22428

ALIGNMENTS

RESULT 1

AAW99559 AAW99559 standard; peptide: 17 AA.

XX AC AAW99559;

XX DT 22-JUN-1999 (first entry)

XX DE Immunoglobulin IgG2a CDR3-derived peptide #1.

XX KW Primer; PCR; amplification; immunoglobulin; IgG2a; repeat motif; antibody; cell penetration; vector; gene therapy; antigen; vaccination.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN FR2766826-A1.

XX PD 05-FEB-1999.

XX XX 04-AUG-1997; 97FR-0009972.

XX PR 04-AUG-1997; 97FR-0009972.

XX PA (INSP) INST PASTEUR.

XX PI Avrameas A, Avrameas S, Buttin G, Ternynck T;

XX DR WPI; 1999-156194/14.

XX PT New polypeptide including sequence from single antibody chain and able to penetrate a cell - used as vector for delivering attached components, e.g. nucleic acid or antigen, to cells, useful in gene therapy and vaccination

PT Heavy chain framew

XX PS Example 2; Page 19; 36pp; French.

CC This sequence corresponds to a peptide derived from the complementary

CC determining region 3 (CDR3) of an immunoglobulin IgG2a protein and is

CC used in the production of a polypeptide that (i) comprises a unique or

CC repeated peptide motif; (ii) includes a sequence consisting of one or

CC more different antibody fragments and (iii) can penetrate into cells.

CC The polypeptides are vectors for delivering a substance to cells

CC (in vivo, in vitro or ex vivo), particularly for use as pharmaceutical

CC (gene therapy, or where the substance is an antigen, for vaccination,

CC in which case the polypeptide acts effectively as an adjuvant).

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 98; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.5e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TRQYKYNKRAMDYWGQGT 17

Db 1 trqkynkrandywgqgt 17

RESULT 2

AAW99561

ID AAW99561 standard; peptide; 17 AA.

AC AAW99561;

XX 22-JUN-1999 (first entry)

XX Immunoglobulin IgG2a CDR3-derived peptide #3.

XX Primer; PCR; amplification; immunoglobulin; IgG2a; repeat motif;

XX antibody; cell penetration; vector; gene therapy; antigen; vaccination.

XX Synthetic.

XX Homo sapiens.

XX FR2766826-A1.

XX 05-FEB-1999.

XX 04-AUG-1997; 97FR-0009972.

XX 04-AUG-1997; 97FR-0009972.

XX (INSP) INST PASTEUR.

XX Avrameas A, Avrameas S, Buttin G, Ternynck T;

XX WPI; 1999-156194/14.

XX New polypeptide including sequence from single antibody chain and

XX able to penetrate a cell - used as vector for delivering attached

XX components, e.g. nucleic acid or antigen, to cells, useful in gene

XX therapy and vaccination

XX Example 2; Page 19; 36pp; French.

XX This sequence corresponds to a peptide derived from the complementary

XX determining region 3 (CDR3) of an immunoglobulin IgG2a protein and is

XX used in the production of a polypeptide that (i) comprises a unique or

XX repeated peptide motif; (ii) includes a sequence consisting of one or

XX more different antibody fragments and (iii) can penetrate into cells.

XX The polypeptides are vectors for delivering a substance to cells

XX (in vivo, in vitro or ex vivo), particularly for use as pharmaceutical

XX (gene therapy, or where the substance is an antigen, for vaccination,

XX in which case the polypeptide acts effectively as an adjuvant).

XX SQ Sequence 17 AA;

Query Match 89.8%; Score 88; DB 20; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.3e-06;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TRQYKYNKRAMDYWGQGT 17

Db 1 trqkygkrgmdywgqgt 17

RESULT 3

AAW99562

ID AAW99562 standard; peptide; 18 AA.

XX AAW99562;

XX 22-JUN-1999 (first entry)

XX Immunoglobulin IgG2a CDR3-derived peptide #4.

XX Primer; PCR; amplification; immunoglobulin; IgG2a; repeat motif;

XX antibody; cell penetration; vector; gene therapy; antigen; vaccination.

XX Synthetic.

XX Homo sapiens.

XX FR2766826-A1.

XX 05-FEB-1999.

XX 04-AUG-1997; 97FR-0009972.

XX 04-AUG-1997; 97FR-0009972.

XX (INSP) INST PASTEUR.

XX Avrameas A, Avrameas S, Buttin G, Ternynck T;

XX WPI; 1999-156194/14.

XX New polypeptide including sequence from single antibody chain and

XX able to penetrate a cell - used as vector for delivering attached

XX components, e.g. nucleic acid or antigen, to cells, useful in gene

XX therapy and vaccination

XX Example 2; Page 19; 36pp; French.

XX This sequence corresponds to a peptide derived from the complementary

XX determining region 3 (CDR3) of an immunoglobulin IgG2a protein and is

XX used in the production of a polypeptide that (i) comprises a unique or

XX repeated peptide motif; (ii) includes a sequence consisting of one or

XX more different antibody fragments and (iii) can penetrate into cells.

XX The polypeptides are vectors for delivering a substance to cells

XX (in vivo, in vitro or ex vivo), particularly for use as pharmaceutical

XX (gene therapy, or where the substance is an antigen, for vaccination,

XX in which case the polypeptide acts effectively as an adjuvant).

XX SQ Sequence 18 AA;

Query Match 85.2%; Score 83.5; DB 20; Length 18;

Best Local Similarity 88.9%; Pred. No. 6.2e-06;

Matches 16; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 TRQYKYNKRAMDYWGQGT 17

Db 1 trqkynkrandywgqgt 18

RESULT 4

AAW93079

ID AAW93079 standard; peptide; 159 AA.

XX AAP93079;
AC 15-MAR-1990 (first entry)
DT Heavy chain of monoclonal antibody 6A4.
DE Monoclonal antibody 6A4; heavy chain; Pseudomonas aeruginosa; OMP-1.
KW EP338395-A.
XX 25-OCT-1989.
PD 12-APR-1989; 89EP-0106463.
XX 19-APR-1988; 88DE-3813023.
XX (BEHW) BEHRINGWERKE.
PA Domdey H, Marget M, von Specht BU;
PI WPI; 1989-310861/43.
XX N-PSDB; AAN91645.
XX Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for
PT variable antibody regions.
XX Claim 1; page 6; 7pp; german.
XX The peptide is encoded by the heavy chain of monoclonal antibody 6A4.
CC 6A4 reacts with the OMP-1 protein of all 19 known serotypes of
CC P.aeruginosa. It is used for therapy and diagnosis of infection, and as
CC a carrier for drugs. The antibody is IgG2a subclass.
XX Sequence 159 AA;
SQ

Query Match 65.8%; Score 64.5; DB 10; Length 159;
Best Local Similarity 72.2%; Pred. No. 0.03;
Matches 13; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
QY 1 TRQKYN-KRAMDYWGQGT 17
|| || : |||||
Db 116 trsyynyegamdywgqgt 133

RESULT 5
AAW21841
ID AAW21841 standard; Protein; 140 AA.
XX AAW21841;
XX 18-DEC-1997 (first entry)
DT Heavy chain variable region of KM1257 antibody.
XX
XX Complementarity determining region; CDR; heavy chain; treatment;
KW variable region; murine; mouse; human; interleukin 5; IL-5;
KW receptor; alpha chain; monoclonal antibody; hybridoma; detection;
KW assay; diagnosis; allergic respiratory disease;
KW chronic bronchitis.
XX Mus spp.
OS

Key Location/Qualifiers
FH Key 1..19
FT Peptide /label= sig_peptide
FT Peptide 20..140
FT Peptide /label= mat_peptide
FT Region 50..54
FT Region /label= complementarity_determining_region_1
FT Region 69..85
FT Region /label= complementarity_determining_region_2

Region 118..129
/label= complementarity_determining_region_3
FT WO9710354-AJ;
XX 20-MAR-1997.
PD 11-SEP-1996; 96WO-JP02588.
XX 11-SEP-1995; 95JP-0232384.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX Anazawa H, Furuya A, Hanai N, Iida A, Koike M;
PI Nakamura K, Takatsu K;
XX WPI; 1997-202249/18.
DR N-PSDB; AAT73608.
XX Antibody against alpha-chain of human interleukin 5 receptor -
PT useful for diagnosis and treatment of respiratory allergic diseases,
PT e.g. chronic bronchitis
XX Example 2; Pages 116-117; 238pp; Japanese.
PS The present sequence is the heavy chain variable region of the
XX murine anti-human interleukin 5 receptor alpha chain (hIL-5R alpha)
CC monoclonal antibody (MAB) KM1257. KM1257 is produced by the hybridoma
CC FERM BP-5133, which was prepared by immunising Balb/c mice with
CC hIL-5R alpha, fusing spleen cells obtained from the mice with mouse
CC myeloma P3-U1 cells and screening the resultant hybridomas. The MAB
CC can be used to detect or assay for hIL-5R alpha and cells
CC expressing it on their surface, especially to diagnose allergic
CC respiratory diseases, e.g. chronic bronchitis. It can also be used
CC to treat such diseases.
XX Sequence 140 AA;
SQ

Query Match 65.3%; Score 64; DB 18; Length 140;
Best Local Similarity 91.7%; Pred. No. 0.032;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 NKRAMDYWGQGT 17
|||||||
Db 123 nyramdywgqgt 134

RESULT 6
AAR74940
ID AAR74940 standard; peptide; 119 AA.
XX AAR74940;
XX 19-JAN-1996 (first entry)
DT Immunoglobulin heavy chain of anti-idiotypic antibody against human
XX anticancer antibody.
DE Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
KW complementarity determining region.
XX Mus sp.
OS

Key Location/Qualifiers
FH Key 31..35
FT Region /label= CDR1
FT Region 50..66
FT Region /label= CDR2
FT Region 99..108
FT Region /label= CDR3
XX JP07101999-A.

XX 18-APR-1995.
 XX 06-OCT-1993; 93JP-0272950.
 XX 06-OCT-1993; 93JP-0272950.
 XX (HAGI/) HAGIWARA Y.
 XX WPI; 1995-182987/24.
 XX Novel anti-idiotypic antibody against an human anticancer monoclonal
 PT antibody - and DNA sequences encoding the antibody, useful in
 PT pharmacology, medicine and biochemical fields.
 XX Claim 2; Page 2; 28pp; Japanese.
 XX AAR74940-R74943 are possible heavy chains of a new anti-idiotypic
 CC antibody against a human anticancer monoclonal antibody. This antibody
 CC contains in its heavy chain 3 complementarity determining regions CDR1
 CC (AAR74929-R74931) CDR2 (AAR74932-R74935) and CDR3 (AAR74936-R74939),
 CC this is also true of the light chain which has its own CDR1
 CC (AAR74944-R74946 and AAR85774), CDR2 (AAR74947-R74949) and CDR3
 CC (AAR74950-R74954). The antibody and DNA encoding it are useful in
 CC pharmacological, medical and biochemical fields.
 XX Sequence 119 AA;
 SQ

Query Match 63.3%; Score 62; DB 16; Length 119;
 Best Local Similarity 52.9%; Pred. No. 0.053;
 Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TRQYKRAMDYWGQGT 17
 |:::|: :|||||
 Db 97 tkeydydtidywgqgt 113

RESULT 7
 AAW01578
 ID AAW01578 standard; Protein; 119 AA.
 XX AAW01578;
 AC AAW01578;
 XX 22-AUG-1997 (first entry)
 DT Lead binding Mab 8E7 heavy chain variable region.
 DE Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
 KW pharmaceutical; health care; skin treatment; pesticide; herbicide;
 KW heavy metal.
 XX Mus musculus.
 OS WO9639518-AL.
 PN 12-DEC-1996.
 XX 05-JUN-1996; 96WO-US09258.
 PF 10-OCT-1995; 95US-0541373.
 XX 05-JUN-1995; 95US-0462798.
 PR (BION-) BIONEERASKA INC.
 XX Lopez O, Murray PJ, Wylie DE;
 PI WPI; 1997-043140/04.
 XX N-PSDB; AAT58252.
 XX DNA encoding heavy metal binding polypeptide sequences - used for
 PT detecting, removing, adding or neutralising heavy metals, such as
 PT lead cations

XX Claim 12; Page 59; 125pp; English.
 XX The present sequence represents the heavy chain variable region for
 CC monoclonal antibody (Mab) 8E7, which immunoreacts with a lead cation.
 CC The sequence was derived from RNA isolated from mouse hybridoma cells.
 CC The protein can be used for binding heavy metals, such as lead cations.
 CC It can be used for detecting, removing, adding or neutralising the
 CC heavy metals in biological and inanimate systems. It can be used in
 CC e.g. aqueous liquid systems, in biological or environmental systems or
 CC in such compositions as perfumes, cosmetics, pharmaceuticals, health
 CC care products, skin treatment products, pesticides, herbicides,
 CC solvents used in the production of semi-conductor and integrated
 CC circuit components and production materials for electronic components.
 CC The products can provide for applications involving minute amounts of
 CC specific heavy metals.
 XX Sequence 119 AA;
 SQ

Query Match 63.3%; Score 62; DB 18; Length 119;
 Best Local Similarity 68.8%; Pred. No. 0.053;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2 RQYKRAMDYWGQGT 17
 | | :|||||
 Db 98 rhygygyamdywgqgt 113

RESULT 8
 AAR74960
 ID AAR74960 standard; Protein; 133 AA.
 XX AAR74960;
 AC AAR74960;
 XX 02-FEB-1996 (first entry)
 DT Anti-idiotypic antibody Idio3 clone 3cB1.
 DE Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
 KW complementarity determining region.
 KW Mus sp.
 XX Key Location/Qualifiers
 FH Peptide 1..9
 FT /label= signal_peptide
 XX JP07101999-A.
 PN 18-APR-1995.
 XX 06-OCT-1993; 93JP-0272950.
 PF 06-OCT-1993; 93JP-0272950.
 XX (HAGI/) HAGIWARA Y.
 XX WPI; 1995-182987/24.
 DR N-PSDB; AAQ90425.
 XX Novel anti-idiotypic antibody against an human anticancer monoclonal
 PT antibody - and DNA sequences encoding the antibody, useful in
 PT pharmacology, medicine and biochemical fields.
 XX Example 5; Page 13; 28pp; Japanese.
 PS AAR74960-R74969 are clones of the anti-idiotypic antibodies Idio3,
 CC Idio17, Idio20, Idio27 and Idio33 against a human anticancer monoclonal
 CC antibody. These antibodies and DNA encoding them are useful in
 CC pharmacological, medical and biochemical fields of research.
 XX Sequence 133 AA;
 SQ

Query Match 63.3%; Score 62; DB 16; Length 133;
 Best Local Similarity 52.9%; Pred. No. 0.059; 3; Indels 0; Gaps 0;
 Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 TROKYNKRAMDYWGQGT 17
 Db 106 tkeeydydtldywgqgt 122

RESULT 9

AAR74961
 ID AAR74961 standard; Protein; 135 AA.

XX AC AAR74961;

DT 02-FEB-1996 (first entry)

DE Anti-idiotypic antibody Idio17 clone 17GB7.

XX Antibody; cancer; anti-idiotypic; CDR; heavy chain; light chain;
 K Immunoglobulin; complementarity determining region.

XX OS Mus sp.

XX Key Location/Qualifiers
 FH Peptide 1..10
 FT /label= signal_peptide
 FT

XX JP07101999-A.

XX 18-APR-1995.

XX 06-OCT-1993; 93JP-0272950.

XX 06-OCT-1993; 93JP-0272950.

XX (HAGI/) HAGIWARA Y.

XX WPI; 1995-182987/24.

DR N-PSDB; AAQ90426.

XX Novel anti-idiotypic antibody against an human anticancer monoclonal
 PT antibody - and DNA sequences encoding the antibody, useful in
 PT pharmacology, medicine and biochemical fields.

XX Example 5; Page 14; 28pp; Japanese.

XX AAR74960-R74969 are clones of the anti-idiotypic antibodies Idio3,
 C Idio17, Idio20, Idio27 and Idio33 against a human anticancer monoclonal
 CC antibody. These antibodies and DNA encoding them are useful in
 CC pharmacological, medical and biochemical fields of research.

XX SQ Sequence 135 AA;

Query Match 63.3%; Score 62; DB 16; Length 135;
 Best Local Similarity 52.9%; Pred. No. 0.06;
 Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 TROKYNKRAMDYWGQGT 17
 Db 107 tkeeydydtldywgqgt 123

RESULT 10

AAY43867

ID AAY43867 standard; Peptide; 143 AA.

XX AC AAY43867;

DT 11-FEB-2000 (first entry)

XX Heavy chain (VH) gene sequence of Bacillus anthracis antibody 24-2.
 DE Heavy chain; VH; IgG; monoclonal antibody; spore; Bacillus;
 KW VH gene usage; anthrax.

XX OS Mus sp.

XX WO9955842-A1.

XX 04-NOV-1999.

XX 27-APR-1999; 99WO-US09122.

XX 29-APR-1998; 98US-0069628.

XX (UABR-) UAB RES FOUND.

XX Kearney JF;

XX WPI; 2000-013435/01.

XX Monoclonal antibody specific for Bacillus spores, used to detect
 PT anthrax

XX Example 13; Page 54; 64pp; English.

XX AAY43862-75 represent the amino acid sequences of the heavy chain
 CC (VH) gene sequences from antibodies against Bacillus anthracis
 CC spores. The antibodies are produced by different hybridomas. The
 CC specification describes monoclonal antibodies (especially IgG
 CC antibodies) which are highly specific and can discriminate between the
 CC spores of the Bacillus family. The antibodies are produced by exposing
 CC mice to Bacillus spores. The humoral immune response to Bacillus spores
 CC shows a conservation of VH gene usage which is distinct for each spore.
 CC Peptide fragments derived from the antibodies are also capable of
 CC binding spores. The monoclonal antibody, and peptide fragments of it, can
 CC be used to detect Bacillus spores in a field sample. It is particularly
 CC uses for detecting anthrax in a field sample.

XX SQ Sequence 143 AA;

Query Match 63.3%; Score 62; DB 21; Length 143;
 Best Local Similarity 68.8%; Pred. No. 0.063;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 RQKYNKRAMDYWGQGT 17
 Db 90 rqqrrryamdywgqgt 105

RESULT 11

AAY43857

ID AAY43857 standard; Peptide; 144 AA.

XX AC AAY43857;

XX 11-FEB-2000 (first entry)

XX Heavy chain framework 3 region of antibodies from hybridoma a05.
 KW Heavy chain; VH; IgG; monoclonal antibody; spore; Bacillus;
 KW VH gene usage; anthrax; framework 3.

XX OS Mus sp.

XX WO9955842-A1.

XX 04-NOV-1999.

XX 27-APR-1999; 99WO-US09122.

PR 29-APR-1998; 98US-0069628.
 PA (UABR-) UAB RES FOUND.
 XX Kearney JF;
 XX WPI; 2000-013435/01.
 XX Monoclonal antibody specific for Bacillus spores, used to detect
 PT anthrax
 XX
 XX Example 10; Page 46-47; 64pp; English.
 XX
 XX AAY43851-61 represent the amino acid sequences of the framework 3 (FR3)
 CC region of heavy chains from antibodies against Bacillus subtilis
 CC spores. The antibodies are produced by different hybridomas. The
 CC specification describes monoclonal antibodies (especially IgG
 CC antibodies) which are highly specific and can discriminate between the
 CC spores of the Bacillus family. The antibodies are produced by exposing
 CC mice to Bacillus spores. The humoral immune response to Bacillus spores
 CC shows a conservation of VH gene usage which is distinct for each spore.
 CC Peptide fragments derived from the antibodies are also capable of
 CC binding spores. The monoclonal antibody, and peptide fragments of it, can
 CC be used to detect Bacillus spores in a field sample. It is particularly
 CC uses for detecting anthrax in a field sample.
 XX
 XX Sequence 144 AA;

Query Match 63.3%; Score 62; DB 21; Length 144;
 Best Local Similarity 83.3%; Pred. No. 0.063;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 NKRANDYWGQGT 17
 Db 95 skraidywgqgt 106
 :|||:|||||

RESULT 12
 AAY91026
 ID AAY91026 standard; Protein; 436 AA.
 XX
 XX AAY91026;
 AC
 XX
 XX 05-SEP-2000 (first entry)
 XX
 XX Apoptobody3sc fusion protein SEQ ID NO:8.
 DE Human; Fas antigen; apoptosis; apoptobody3sc; antibody; fusion gene;
 KW medical; pharmaceutical; pharmacological; biochemical.
 KW
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX JP2000102389-A.
 PN
 XX
 XX 11-APR-2000.
 PD
 XX 29-SEP-1998; 98JP-0291441.
 XX
 XX 29-SEP-1998; 98JP-0291441.
 XX
 XX (HAGI/) HAGIWARA Y.
 PA (HAGI/) HAGIWARA H.
 PA
 XX WPI; 2000-332086/29.
 DR N-PSDB; AAA39167.
 XX
 XX Causing apoptosis comprises transfecting fused gene to cell and
 PT reacting cell with idiotypic antibody -
 XX
 XX Disclosure; Page 8-9; 10pp; Japanese.
 PS
 XX

CC The present invention describes a method for causing apoptosis in which
 CC a fused gene consisting of a gene participating to apoptosis and a gene
 CC encoding at least the variable region of anti-idiotypic antibody is
 CC transfected to a cell to express the fused gene and then an idiotype
 CC antibody is reacted with the expressed cell. The method is useful in
 CC medical, pharmaceutical, pharmacological and biochemical fields. The
 CC present sequence represents a fusion protein designated apoptobody3sc,
 CC which is used in the exemplification of the present invention.
 XX
 XX Sequence 436 AA;

Query Match 63.3%; Score 62; DB 21; Length 436;
 Best Local Similarity 52.9%; Pred. No. 0.19;
 Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 TROKYNKRANDYWGQGT 17
 Db 250 tkeedydtldygqgt 266
 :|||:|||||

RESULT 13
 AAR25730
 ID AAR25730 standard; Protein; 119 AA.
 XX
 XX AAR25730;
 AC
 XX
 XX 13-JAN-1993 (first entry)
 DT
 XX
 XX Humanised VH region of the mouse CMV5 antibody.

XX Murine; immunoglobulin; CDR; non immunogenic; cytomegalovirus;
 KW gH; heavy chain; variable region; framework; human; Wol.

XX Mus musculus.
 OS
 XX
 XX Key Location/Qualifiers
 FH Region 31...35 "CDR"
 FT /note= "CDR"
 FT Region 50...66
 FT /note= "CDR"
 FT Region 99...108
 FT /note= "CDR"
 FT Misc-difference 5 /note= "mutated residue"
 FT Misc-difference 24 /note= "mutated residue"
 FT Misc-difference 27 /note= "mutated residue"
 FT Misc-difference 28 /note= "mutated residue"
 FT Misc-difference 30 /note= "mutated residue"
 FT Misc-difference 69 /note= "mutated residue"
 FT Misc-difference 80 /note= "mutated residue"
 FT Misc-difference 97 /note= "mutated residue"
 FT /note= "mutated residue"

XX WO9211018-A.
 PN
 XX 09-JUL-1992.
 PD
 XX 19-DEC-1991; 91WO-US09711.
 XX
 XX 19-DEC-1990; 90US-0634278.
 PR
 XX (PROT-) PROTEIN DESIGN LABS INC.
 PA
 XX Co MS, Coeligh KL, Landolfi NF, Queen CL, Schneider WP;
 PI
 XX WPI; 1992-249842/30.
 XX

XX New immunoglobulin(s) having murine CDRs in human framework
PT regions - have lower antigenicity; useful for treating e.g. HSV,
PT CMV, T-cell disorders, myeloid disorders and auto-immune
PT conditions
XX
XX Claim 40; Fig 27B; 141pp; English.
XX
XX The sequence shows the humanised mature heavy chain variable
CC region of the mouse CMV5 antibody. Murine CDRs were used
CC in a human Wol framework to produce a pure humanised immunoglobulin
CC (Ig) which is capable of binding to the gH glycoprotein of
CC cytomegalovirus. The Ig is non immunogenic, due to the human
CC framework, and has a strong affinity for its predetermined
CC antigen. They can be produced in large quantities via recombinant
CC DNA and monoclonal antibody technology. The humanised Igs may be
CC used alone or in combination with chemotherapeutic agents such as
CC non-steroidal anti-inflammatory drugs or immunosuppressants.
CC See also AAR25721-32.
XX
XX Sequence 119 AA;

Query Match 62.2%; Score 61; DB 13; Length 119;
Best Local Similarity 58.8%; Pred. No. 0.074;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRQYKYNKRAMDYWGQGT 17
||: : : |||||
Db 97 trgrfdysmdywgqgt 113

RESULT 14

AAB69679
ID AAB69679 standard; Protein; 119 AA.

XX AAB69679;

DT 30-APR-2001 (first entry)

DE Murine CMV5 antibody heavy chain SEQ ID NO: 64.

XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
KW light chain; graft versus host disease; transplant; autoimmune disease;
KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

XX Mus sp.

OS JS6180370-B1.

PN 30-JAN-2001.

XX 07-JUN-1995; 95US-0484537.

XX 28-DEC-1988; 88US-0290975.

XX 13-FEB-1989; 89US-0310252.

XX 28-SEP-1990; 90US-0590274.

XX 19-DEC-1990; 90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Queen CL, Selick HE;

XX WPI; 2001-190856/19.

XX Producing humanized immunoglobulin, involves producing a cell
PT containing DNA segments encoding humanized heavy and light chain
PT variable regions, and expressing the DNA segments in the cell -
XX

PS Disclosure: Fig 6; 145pp; English.

XX The present invention describes a method of producing humanised

CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
CC humanised version of an immunoglobulin. This is obtained by comparing a
CC donor and human immunoglobulin and producing a combined antibody which
CC contains part of each. These are useful in the treatment of
CC graft-versus-host disease, transplant rejection, autoimmune diseases such
CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
CC and systemic lupus erythematosus, herpes infections, CMV virus infections
CC and myeloid leukaemia. The present sequence is an antibody used to
CC demonstrate the method of the invention.

XX Sequence 119 AA;

Query Match 62.2%; Score 61; DB 22; Length 119;
Best Local Similarity 58.8%; Pred. No. 0.074;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRQYKYNKRAMDYWGQGT 17
||: : : |||||
Db 97 trgrfdysmdywgqgt 113

RESULT 15

AAB69680

ID AAB69680 standard; Protein; 119 AA.

XX AAB69680;

DT 30-APR-2001 (first entry)

DE Humanised CMV5 antibody heavy chain SEQ ID NO: 65.

XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
KW light chain; graft versus host disease; transplant; autoimmune disease;
KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

XX Mus sp.

OS Homo sapiens.

XX US6180370-B1.

XX 30-JAN-2001.

XX 07-JUN-1995; 95US-0484537.

XX 28-DEC-1988; 88US-0290975.

XX 13-FEB-1989; 89US-0310252.

XX 28-SEP-1990; 90US-0590274.

XX 19-DEC-1990; 90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Queen CL, Selick HE;

XX WPI; 2001-190856/19.

XX Producing humanized immunoglobulin, involves producing a cell
PT containing DNA segments encoding humanized heavy and light chain
PT variable regions, and expressing the DNA segments in the cell -
XX

PS Disclosure: Fig 6; 145pp; English.

XX The present invention describes a method of producing humanised
CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
CC humanised version of an immunoglobulin. This is obtained by comparing a
CC donor and human immunoglobulin and producing a combined antibody which
CC contains part of each. These are useful in the treatment of
CC graft-versus-host disease, transplant rejection, autoimmune diseases such
CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
CC and systemic lupus erythematosus, herpes infections, CMV virus infections
CC and myeloid leukaemia. The present sequence is an antibody used to
CC demonstrate the method of the invention.

XX
SQ

Sequence 119 AA;

Query Match 62.2%; Score 61; DB 22; Length 119;
Best Local Similarity 58.8%; Pred. No. 0.074; 4; Indels 0; Gaps 0;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 TROKYNKRAMDYWGQGT 17

||: : :|||||||
Db 97 trgrfdysmdywgqgt 113

Search completed: June 27, 2001, 11:29:17
Job time: 57 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2001, 11:28:20 ; Search time 11.81 seconds
(without alignments)
28.997 Million cell updates/sec

Title: US-09-497-997B-1

Perfect score: 98
Sequence: 1 TRQYKRAMDYWGQT 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 2014635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/6C_COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/6D_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	65.3	140	3	US-08-836-561-23
2	62	63.3	119	4	US-08-767-128-6
3	61	62.2	115	2	US-08-379-057-31
4	61	62.2	118	2	US-08-379-057-30
5	61	62.2	119	1	US-07-634-278-64
6	61	62.2	119	1	US-07-634-278-65
7	61	62.2	119	1	US-07-634-278-89
8	61	62.2	119	1	US-08-477-728-64
9	61	62.2	119	1	US-08-477-728-65
10	61	62.2	119	1	US-08-477-728-89
11	61	62.2	119	1	US-08-474-040-64
12	61	62.2	119	1	US-08-474-040-65
13	61	62.2	119	1	US-08-474-040-89
14	61	62.2	119	1	US-08-487-200-64
15	61	62.2	119	1	US-08-487-200-65
16	61	62.2	119	1	US-08-487-200-89
17	61	62.2	119	4	US-08-484-537-64
18	61	62.2	119	4	US-08-484-537-65
19	61	62.2	119	4	US-08-484-537-89
20	61	62.2	138	1	US-07-634-278-85
21	61	62.2	138	1	US-08-477-728-85
22	61	62.2	138	1	US-08-474-040-85
23	61	62.2	138	1	US-08-487-200-85
24	61	62.2	138	2	US-08-379-057-14
25	61	62.2	138	4	US-08-484-537-85
26	60	61.2	118	2	US-08-553-497A-16
27	59	60.2	118	2	US-08-888-366-4

28	59	60.2	118	5	PCT-US93-08435-10	Sequence 10, Appl
29	59	60.2	122	5	PCT-US93-08435-12	Sequence 12, Appl
30	59	60.2	122	5	PCT-US93-08435-14	Sequence 14, Appl
31	59	60.2	122	5	PCT-US93-08435-43	Sequence 43, Appl
32	59	60.2	124	4	US-08-767-128-38	Sequence 38, Appl
33	58	59.2	115	3	US-08-881-037-22	Sequence 22, Appl
34	58	59.2	121	3	US-08-881-037-67	Sequence 67, Appl
35	58	59.2	123	2	US-08-561-521-9	Sequence 9, Appl
36	58	59.2	123	2	US-08-561-521-11	Sequence 11, Appl
37	58	59.2	123	5	PCT-US93-01219-9	Sequence 9, Appl
38	58	59.2	123	5	PCT-US93-01219-11	Sequence 11, Appl
39	58	59.2	140	2	US-08-561-521-4	Sequence 4, Appl
40	58	59.2	140	5	PCT-US93-01219-4	Sequence 4, Appl
41	58	59.2	142	2	US-08-561-521-17	Sequence 17, Appl
42	58	59.2	142	5	PCT-US93-01219-17	Sequence 17, Appl
43	56.5	57.7	222	2	US-08-737-129A-6	Sequence 6, Appl
44	56	57.1	116	1	US-08-401-908-1	Sequence 1, Appl
45	56	57.1	116	4	US-08-397-411-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-836-561-23
; Sequence 23, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, No. 6018032uo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; RECEPTOR Alpha Chain
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal

US-08-836-561-23

Query Match 65.3%; Score 64; DB 3; Length 140;
Best Local Similarity 91.7%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 NKRAMDYWGQGT 17
| | | | | | | | | |
Db 123 NYRAMDYWGQGT 134

RESULT 2

US-08-767-128-6
; Sequence 6, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-6

Query Match 63.3%; Score 62; DB 4; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 RQYNKRAMDYWGQGT 17
| | | | | | | | | |
Db 98 RHHYGYAMDYWGQGT 113

RESULT 3

US-08-379-057-31
; Sequence 31, Application US/08379057
; Patent No. 5876950
; GENERAL INFORMATION:
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Gilliland, Lisa K.
; APPLICANT: Gordon, Marcia L.
; APPLICANT: Bajorath, Jurgan
; APPLICANT: Aruffo, Alejandro A.
; TITLE OF INVENTION: Monoclonal Antibodies Specific For
; TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use
; TITLE OF INVENTION: In Diagnosis and Therapy
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,057
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: QN0133-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 727-3670
; TELEFAX: (206) 727-3601
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-379-057-31

Query Match 62.2%; Score 61; DB 2; Length 115;
Best Local Similarity 76.9%; Pred. No. 0.023;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 YNKRAMDYWGQGT 17
| | | | | | | | | |
Db 98 YDSYAMDYWGQGT 110

RESULT 4

US-08-379-057-30
; Sequence 30, Application US/08379057
; Patent No. 5876950
; GENERAL INFORMATION:

APPLICANT: Siadak, Anthony W.
APPLICANT: Hollenbaugh, Diane L.
APPLICANT: Gilliland, Lisa K.
APPLICANT: Gordon, Marcia L.
APPLICANT: Bajorath, Jurgen
APPLICANT: Aruffo, Alejandro A.
TITLE OF INVENTION: Monoclonal Antibodies Specific For
TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use
TITLE OF INVENTION: In Diagnosis and Therapy
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,057
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0133-
TELEPHONE: (206) 727-3670
TELEFAX: (206) 727-3601
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-379-057-30

Query Match 62.2%; Score 61; DB 2; Length 118;
Best Local Similarity 76.9%; Pred. No. 0.024;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 5 YNKRMDYWGQGT 17
I: |||||
D 101 YDSYMDYWGQGT 113
RESULT 5
US-07-634-278-64
Sequence 64, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-64
Query Match 62.2%; Score 61; DB 1; Length 119;
Best Local Similarity 58.8%; Pred. No. 0.024;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 TRQYKRAMDYWGQGT 17
I: |||||
Db 97 TRGRDYSMDYWGQGT 113
RESULT 6
US-07-634-278-65
Sequence 65, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 65:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-65

Query Match 62.2%; Score 61; DB 1; Length 119;
Best Local Similarity 58.8%; Pred. No. 0.024;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TRQYKRAMDYWGQGT 17
||: : |||||
Db 97 TRGRFDYSMDYWGQGT 113

RESULT 7

US-07-634-278-89
Sequence 89, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Map Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-89

Query Match 62.2%; Score 61; DB 1; Length 119;
Best Local Similarity 58.8%; Pred. No. 0.024;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TRQYKRAMDYWGQGT 17
||: : |||||
Db 97 TRGRFDYSMDYWGQGT 113

RESULT 8

US-08-477-728-64
Sequence 64, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids

;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-477-728-64

Query Match 62.2%; Score 61; DB 1; Length 119;
Best Local Similarity 58.8%; Pred. NO. 0.024;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 TRQYKRAMDYWGQGT 17
||: : |||||
Db 97 TRGRDYSMDYWGQGT 113

RESULT 9
US-08-477-728-65
; Sequence 65, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-65

Query Match 62.2%; Score 61; DB 1; Length 119;
Best Local Similarity 58.8%; Pred. NO. 0.024;

Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 TRQYKRAMDYWGQGT 17
||: : |||||
Db 97 TRGRDYSMDYWGQGT 113

RESULT 10
US-08-477-728-89
; Sequence 89, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-89

Query Match 62.2%; Score 61; DB 1; Length 119;
Best Local Similarity 58.8%; Pred. NO. 0.024;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 TRQYKRAMDYWGQGT 17
||: : |||||
Db 97 TRGRDYSMDYWGQGT 113

RESULT 11
US-08-474-040-64

; Sequence 64, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-474-040-64

Query Match 62.2%; Score 61; DB 1; Length 119;
Best Local Similarity 58.8%; Pred. No. 0.024;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TRQYNKRAMDYWGQGT 17
Db 97 TRRGFRDYSMDYWGQGT 113

RESULT 12
US-08-474-040-65
; Sequence 65, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.

; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-474-040-65

Query Match 62.2%; Score 61; DB 1; Length 119;
Best Local Similarity 58.8%; Pred. No. 0.024;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TRQYNKRAMDYWGQGT 17
Db 97 TRRGFRDYSMDYWGQGT 113

RESULT 13
US-08-474-040-89
; Sequence 89, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue

;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: US
;; ZIP: 94301
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/474,040
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/634,278
;; FILING DATE: 19-DEC-1990
;; APPLICATION NUMBER: US 07/590,274
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/310,252
;; FILING DATE: 13-FEB-1989
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002600
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 89:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-474-040-89

Query Match 62.2%; Score 61; DB 1; Length 119;
Best Local Similarity 58.8%; Pred. No. 0.024;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 TRQYKRAMDYWGQGT 17
|||: : |||||
Db 97 TRGFRDYSMDYWGQGT 113
RESULT 14
US-08-487-200-64
; Sequence 64, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/487,200
;; FILING DATE: 7-JUN-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/634,278
;; FILING DATE: 19-DEC-1990
;; APPLICATION NUMBER: US 07/590,274
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/310,252
;; FILING DATE: 13-FEB-1989
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002610
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 64:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-487-200-64

Query Match 62.2%; Score 61; DB 1; Length 119;
Best Local Similarity 58.8%; Pred. No. 0.024;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 TRQYKRAMDYWGQGT 17
|||: : |||||
Db 97 TRGFRDYSMDYWGQGT 113
RESULT 15
US-08-487-200-65
; Sequence 65, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-65

Query Match 62.2%; Score 61; DB 1; Length 119;
Best Local Similarity 58.8%; Pred. No. 0.024;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 TRQYKRAMDYWGQGT 17
||: : |||||
Db 97 TRGFRDYSMDYWGQGT 113

Search completed: June 27, 2001, 11:28:37
Job time: 17 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2001, 11:28:40 ; Search time 21.08 Seconds
(without alignments)
106.698 Million cell updates/sec

Title: US-09-497-997B-1

Perfect score: 98

Sequence: 1 TRQYKRAMDYWGQGT 17

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16.*

1: sp_bacteria.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_unclassified.*

13: sp_vertebrate.*

14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58.5	59.7	110	11 Q9JL77	Q9JL77 mus musculus
2	56	57.1	117	11 Q9QXE9	Q9QXE9 mus musculus
3	55.5	56.6	112	4 Q9HCC1	Q9HCC1 homo sapien
4	55	56.1	109	11 Q9JL75	Q9JL75 mus musculus
5	53	54.1	118	4 Q9UL72	Q9UL72 homo sapien
6	50	51.0	321	2 Q9KR64	Q9KR64 vibrio chol
7	49	50.0	147	4 Q9Y509	Q9Y509 homo sapien
8	48	49.0	119	5 Q9GY22	Q9GY22 schistosoma
9	46	46.9	109	11 Q9JL85	Q9JL85 mus musculus
10	46	46.9	113	4 Q9UL90	Q9UL90 homo sapien
11	46	46.9	114	11 Q9JL81	Q9JL81 mus musculus
12	46	46.9	117	11 Q9QXE0	Q9QXE0 mus musculus
13	46	46.9	118	11 Q9Z1C4	Q9Z1C4 mus musculus
14	46	46.9	119	4 Q9UL73	Q9UL73 homo sapien
15	46	46.9	121	4 Q9UL96	Q9UL96 homo sapien
16	46	46.9	122	4 Q9UL84	Q9UL84 homo sapien
17	46	46.9	122	4 Q9UL75	Q9UL75 homo sapien
18	46	46.9	124	4 Q9UL92	Q9UL92 homo sapien
19	46	46.9	314	2 P74237	P74237 synecocyst

20	46	46.9	384	4 Q9UP60	Q9UP60 homo sapien
21	45	45.9	1031	2 Q9WXJ2	Q9WXJ2 psychromona
22	44	44.9	131	4 Q9UL88	Q9UL88 homo sapien
23	44	44.9	377	7 Q9GIW6	Q9GIW6 ictalurus p
24	44	44.9	401	5 Q91602	Q91602 caenorhabdi
25	44	44.9	436	10 Q22949	Q22949 arabidopsis
26	44	44.9	658	11 Q9QWS9	Q9QWS9 mus musculu
27	44	44.9	739	2 Q9X687	Q9X687 salmonella
28	43	43.9	27	14 Q78983	Q78983 human immun
29	43	43.9	27	14 Q78989	Q78989 human immun
30	43	43.9	118	4 Q9UL91	Q9UL91 homo sapien
31	43	43.9	196	14 Q9WGP1	Q9WGP1 human immun
32	43	43.9	218	14 Q9YIU8	Q9YIU8 human immun
33	43	43.9	218	14 Q9WBH8	Q9WBH8 human immun
34	43	43.9	328	14 Q9EL95	Q9EL95 human immun
35	43	43.9	328	14 Q9EID8	Q9EID8 human immun
36	43	43.9	328	14 Q9EHY2	Q9EHY2 human immun
37	43	43.9	328	14 Q9EGX2	Q9EGX2 human immun
38	43	43.9	328	14 Q9EFW2	Q9EFW2 human immun
39	43	43.9	328	14 Q9EE99	Q9EE99 human immun
40	43	43.9	328	14 Q9ECP1	Q9ECP1 human immun
41	43	43.9	328	14 Q9ECC1	Q9ECC1 human immun
42	43	43.9	416	4 Q9NPP6	Q9NPP6 homo sapien
43	43	43.9	566	2 P94189	P94189 alicalignes
44	43	43.9	1095	5 Q01478	Q01478 caenorhabdi
45	42	42.9	118	4 Q9UL74	Q9UL74 homo sapien

ALIGNMENTS

RESULT 1					
Q9JL77					
ID	Q9JL77	PRELIMINARY;	PRT;	110 AA.	
AC	Q9JL77;				
DT	01-OCT-2000 (Tremblrel. 15, Created)				
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)				
DT	01-MAR-2001 (Tremblrel. 16, Last annotation update)				
DE	ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RC	STRAIN=DKA/2;				
RA	Maikael S., Liao L., Cunningham M.W., Diamond B.;				
RT	*Characterization of cross-reactive monoclonal anti-myosin/anti-n-				
RT	acetyl-glucosamine antibodies from mice with autoimmune myocarditis.;				
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: AF206029; AAF69327.1; -				
DR	InterPro: IPR003006; -				
DR	InterPro: IPR003596; -				
DR	Pfam: PF00047; ig; 1.				
DR	SMART: SM00406; IGV; 1.				
FT	NON_TER 1				
FT	NON_TER 110 110				
SQ	SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;				

Query Match 59.7%; Score 58.5; DB 11; Length 110;
Best Local Similarity 75.0%; Pred. No. 0.027; 2; Indels 1; Gaps 1;
Matches 12; Conservative 1; Mismatches 1;

QY 2 RQYKRAMDYWGQGT 17
||: | |||||
Db 90 RQRN-YAMDYWGQGT 104

RESULT 2
Q9QXE9 PRELIMINARY; PRT; 117 AA.
ID Q9QXE9
AC Q9QXE9;

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RL acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206031; AAF69329.1; -
DR InterPro; IPR003006; -
DR InterPro; IPR003596; -
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 109
FT SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;
SQ

Query Match 56.1%; Score 55; DB 11; Length 109;
Best Local Similarity 75.0%; Pred. No. 0.099;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 NKRAMDYWGQGT 17
Db 92 NYRGFDYWGQGT 103
I : | | | | | | | |

RESULT 5
ID Q9UL72 PRELIMINARY; PRT; 118 AA.
AC Q9UL72;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF035042; AAD56278.1; -
DR HSSP: P01772; 2FBA.
DR InterPro; IPR003006; -
DR InterPro; IPR003596; -
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 118
FT SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;
SQ

Query Match 54.1%; Score 53; DB 4; Length 118;
Best Local Similarity 50.0%; Pred. No. 0.23;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 RQYKNRAMDYWGQGT 17
Db 97 RDRGEFEDYWGQGT 112
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RESULT 6
Q9KR64

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ID Q9KR64 PRELIMINARY: PRT: 321 AA.
AC Q9KR64;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE C4-DICARBOXYLATE-BINDING PERIPLASMIC PROTEIN.
GN VC1779.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae";
RL Nature 406:477-483(2000).
DR EMBL; AE004255; AAF94928.1; -.
DR TIGR; VC1779; -.
SQ SEQUENCE 321 AA; 35982 MW; C1A44BB820F595F0 CRC64;

Query Match 51.0%; Score 50; DB 2; Length 321;
Best Local Similarity 60.0%; Pred. No. 2.2;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 QYKRAMDYWGQGT 17
DB 132 QKFNWRALDTWYNGT 146
RESULT 7
QY509 PRELIMINARY: PRT: 147 AA.
AC QY509;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE V3 PROTEIN (FRAGMENT).
GN V3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers";
RL Leukemia 9:1948-1953(1995).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; S80860; AAD14339.1; -.
DR HSP; P01772; 2F8A
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; 1g; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;

Query Match 50.0%; Score 49; DB 4; Length 147;
Best Local Similarity 61.5%; Pred. No. 1.3;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 5 YNKRAMDYWGQGT 17
DB 108 YYAGIDYWGQGT 120
RESULT 8
Q9GVZ2 PRELIMINARY: PRT: 119 AA.
ID Q9GVZ2;
AC Q9GVZ2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatidae; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAG01452.1; -.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

Query Match 49.0%; Score 48; DB 5; Length 119;
Best Local Similarity 87.5%; Pred. No. 1.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 MDYWGQGT 17
DB 106 LDYWGQGT 113
RESULT 9
Q9JL85 PRELIMINARY: PRT: 109 AA.
ID Q9JL85;
AC Q9JL85;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206021; AAF69319.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; 1g; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;

Query Match 46.9%; Score 46; DB 11; Length 109;

Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 DYWGQGT 17

|||||||

Db 97 DYWGQGT 103

RESULT 10

Q9UL90 ID Q9UL90 PRELIMINARY; PRT; 113 AA.

AC Q9UL90;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.;"

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

CC DOMAIN.

DR EMBL; AF035024; AAD56260.1; -

DR InterPro; IPR003006; -

DR InterPro; IPR003596; -

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

FT NON_TER 1

FT NON_TER 113

SQ SEQUENCE 113 AA; 13437 MW; ED57FDD19086D07F CRC64;

Query Match 46.9%; Score 46; DB 4; Length 113;

Best Local Similarity 53.8%; Pred. No. 3.1;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 YNKRMDYWGQGT 17

|||||||

Db 95 YCAKDLNYWGQGT 107

RESULT 11

Q9JL81

ID Q9JL81 PRELIMINARY; PRT; 114 AA.

AC Q9JL81;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C;

RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;

RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-

RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.;"

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF206025; AAF69323.1; -

DR InterPro; IPR003006; -

DR InterPro; IPR003596; -

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

FT NON_TER 1
NON_TER 114
SEQUENCE 114 AA; 12829 MW; 404885FDE8BA56F8 CRC64;

Query Match 46.9%; Score 46; DB 11; Length 114;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 DYWGQGT 17

|||||||

Db 102 DYWGQGT 108

RESULT 12

Q9QXF0

ID Q9QXF0 PRELIMINARY; PRT; 117 AA.

AC Q9QXF0;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Clemens A., Rademaekers A., Specht C., Koelsch E.;

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ225171; CAB65236.1; -

DR InterPro; IPR003006; -

DR InterPro; IPR003596; -

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

FT NON_TER 1

FT NON_TER 117

SQ SEQUENCE 117 AA; 13060 MW; DB16AD0858A47E4C CRC64;

Query Match 46.9%; Score 46; DB 11; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.2;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 DYWGQGT 17

|||||||

Db 105 DYWGQGT 111

RESULT 13

Q9Z1C4

ID Q9Z1C4 PRELIMINARY; PRT; 118 AA.

AC Q9Z1C4;

DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C;

RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.;

RA Matis L.M., Evans M.J.;

RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric

RT IgG2/4 constant regions block human leukocyte binding to porcine

RT endothelial cells.;"

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

CC DOMAIN.

DR EMBL; U78801; AAD00293.1; -

DR InterPro; IPR003006; -
DR InterPro; IPR003596; -
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;

Query Match 46.9%; Score 46; DB 11; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DYWGQGT 17
Db 106 DYWGQGT 112

RESULT 14
Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
DR EMBL; AF035041; AAD56277.1; -
DR InterPro; IPR003006; -
DR InterPro; IPR003596; -
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;

Query Match 46.9%; Score 46; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DYWGQGT 17
Db 107 DYWGQGT 113

RESULT 15
Q9UL96 PRELIMINARY; PRT; 121 AA.
AC Q9UL96;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
DR EMBL; AF035018; AAD56254.1; -
DR InterPro; IPR003006; -
DR InterPro; IPR003596; -
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CRC64;

Query Match 46.9%; Score 46; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DYWGQGT 17
Db 109 DYWGQGT 115

Search completed: June 27, 2001, 11:33:10
Job time: 270 sec

[Handwritten signature]

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2001, 11:28:55 ; Search time 8.3 Seconds
(without alignments)
70.162 Million cell updates/sec

Title: US-09-497-997b-1

Perfect score: 98

Sequence: 1 TRQYKRAMDYWGQGT 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	56	57.1	136	1 HV16_MOUSE	P01783 mus musculus
2	51	52.0	122	1 HV3G_HUMAN	P01768 homo sapien
3	50	51.0	117	1 HV42_MOUSE	P01812 mus musculus
4	50	51.0	139	1 HV07_MOUSE	P01751 mus musculus
5	49	50.0	136	1 HV15_MOUSE	P01759 mus musculus
6	49	50.0	137	1 HV11_MOUSE	P01755 mus musculus
7	48	49.0	144	1 HV43_MOUSE	P01819 mus musculus
8	47.5	48.5	135	1 HV02_XENLA	P20957 xenopus lae
9	46	46.9	111	1 HV35_MOUSE	P01804 mus musculus
10	46	46.9	116	1 HV3T_HUMAN	P01781 homo sapien
11	46	46.9	118	1 HV39_MOUSE	P01809 mus musculus
12	46	46.9	120	1 HV03_MOUSE	P01747 mus musculus
13	46	46.9	120	1 HV1H_HUMAN	P80421 homo sapien
14	46	46.9	126	1 HV3E_HUMAN	P01772 homo sapien
15	46	46.9	137	1 HV46_MOUSE	P01822 mus musculus
16	46	46.9	140	1 HV02_MOUSE	P01746 mus musculus
17	44.5	45.4	984	1 L100_ADEG1	O64760 avian adeno
18	44	44.9	115	1 HV3S_HUMAN	P01780 homo sapien
19	44	44.9	122	1 HV3H_HUMAN	P01769 homo sapien
20	44	44.9	124	1 HV1E_HUMAN	P01761 homo sapien
21	43.5	44.4	113	1 HV27_MOUSE	P01796 mus musculus
22	43.5	44.4	113	1 HV28_MOUSE	P01797 mus musculus
23	43.5	44.4	113	1 HV29_MOUSE	P01798 mus musculus
24	43.5	44.4	113	1 HV30_MOUSE	P01799 mus musculus
25	43.5	44.4	115	1 HV32_MOUSE	P01801 mus musculus
26	43	43.9	117	1 HV2B_RABIT	P01828 oryctolagus
27	43	43.9	142	1 HV01_RAT	P01805 rattus norv
28	43	43.9	146	1 HV2I_HUMAN	P06331 homo sapien
29	43	43.9	201	1 FABG_BRANA	P27582 brassica na
30	43	43.9	779	1 YU20_ARATH	Q92pvs arabidopsis
31	42.5	43.4	549	1 YST1_CAEEL	Q22000 caenorhabdi
32	42.5	43.4	897	1 APGL_YEAST	P53104 saccharomyc
33	42	42.9	89	1 HV02_HETFR	P04215 heterodontu

Query Match 57.1%; Score 56; DB 1; Length 136;
Best Local Similarity 76.9%; Pred. No. 0.019;

ALIGNMENTS

```
RESULT 1
HV16_MOUSE
ID HV16_MOUSE STANDARD; PRT; 136 AA.
AC P01783:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG HEAVY CHAIN V REGION MOPC 21 PRECURSOR (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Inanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adetugbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; J00522; AAD15290.1; -.
DR PIR; A02066; GIMS21.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1
FT SIGNAL <1 16
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).
FT CONFLICT 89 90 DN -> ND (IN REF. 2).
FT CONFLICT 115 115 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;
```

P01784 canis faml
P01765 homo sapien
P01779 homo sapien
P80419 homo sapien
P01818 homo sapien
P01771 homo sapien
P04438 homo sapien
P50848 bacillus su
P04092 saccharomyc
O01634 canis faml
O43847 homo sapien
P47245 rattus norv

34 42 42.9 114 1 HV01_CANFA
35 42 42.9 115 1 HV3D_HUMAN
36 42 42.9 116 1 HV3R_HUMAN
37 42 42.9 118 1 HV3V_HUMAN
38 42 42.9 121 1 HV2E_HUMAN
39 42 42.9 121 1 HV3J_HUMAN
40 42 42.9 147 1 HV2H_HUMAN
41 42 42.9 501 1 YPWA_BACSU
42 42 42.9 516 1 YJ7_YEAST
43 42 42.9 655 1 IDUA_CANFA
44 42 42.9 1147 1 NRDC_HUMAN
45 42 42.9 1161 1 NRDC_RAT

Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 YNKRMDYWGQGT 17
I :|||||
Db 118 YPYVMDYWGQGT 130

RESULT 2

HV3G_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W.; Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment."
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
DR PIR: A02051; M3HUAM.
DR HSP; P01772; 2IG2.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 52.0%; Score 51; DB 1; Length 122;
Best Local Similarity 66.7%; Pred. No. 0.12;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 NKRAMDYWGQGT 17
: ||:|||||
Db 105 BYRAFNYWGQGT 116

HV42_MOUSE STANDARD; PRT; 117 AA.
AC P01812;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 173.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-104.
RX MEDLINE=72105531; PubMed=5062012;
RA Bourgois A., Fougereau M., de Preval C.;
RT "Sequence of amino acids of the NH 2-terminal region of a
RT mouse-clonal immunoglobulin heavy chain."
RL Eur. J. Biochem. 24:446-455(1972).
RN [2]
RP SEQUENCE OF 105-117.
RX MEDLINE=76091933; PubMed=812695;
RA Rocca-Serra J., Milili M., Fougereau M.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin. Amino-acid sequence of the H4 cyanogen-bromide
RT fragment."

RL Eur. J. Biochem. 59:511-523(1975).
RN [3]
RP SEQUENCE OF 96-117 FROM N.A.
RX MEDLINE=81223769; PubMed=6787590;
RA Gough N.M., Bernard O.;
RT "Sequences of the joining region genes for immunoglobulin heavy
RT chains and their role in generation of antibody diversity."
RL Proc. Natl. Acad. Sci. U.S.A. 78:509-513(1981).
RN [4]
RP DISULFIDE BOND.
RA Bourgois A., Fougereau M.;
RT "Partial amino acid sequence of the variable region of a mouse
RT gamma2a immunoglobulin heavy chain. Evidence for the existence of a
RT third sub-group of variability for the heavy chain pool."
RL FEBS Lett. 8:265-268(1970).
CC -1- MISCELLANEOUS: THIS GAMMA-2A CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
DR PIR: A02082; G2MS73.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT CONFLICT 105 105 N -> D (IN REF. 2).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13051 MW; 156DCCC259380F19 CRC64;

Query Match 51.0%; Score 50; DB 1; Length 117;
Best Local Similarity 88.9%; Pred. No. 0.16;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 AMDYWGQGT 17
||:|||||
Db 103 AMNYWGQGT 111

RESULT 4

HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
DR EMBL; J00529; AAA38170.1; -.
DR PIR: A02034; MHMS18.
DR InterPro; IPR003006; -.

DR Pfam; PF00047; ig: 1.
KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
FT DOMAIN 20 49 FRAMEWORK 1
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC09F465 CRC64;

Query Match 51.0%; Score 50; DB 1; Length 139;
Best Local Similarity 61.5%; Pred. No. 0.19; Mismatches 5; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 5 YNKRAMDYWGQGT 17
DB 121 YGSSYFDYWGQGT 133

RESULT 5

HV15_MOUSE
ID HV15_MOUSE STANDARD; PRT; 136 AA.

AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION BCL1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
by a cloned B-cell lymphoma: a single copy of the VH gene is shared
by two adjacent CH genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).

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DR EMBL; J00494; AAA38130.1; -.
DR PIR; A02042; HVMSB1.
DR InterPro; IPR003006;
DR Pfam; PF00047; ig: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 50.0%; Score 49; DB 1; Length 136;
Best Local Similarity 57.1%; Pred. No. 0.28;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YNKRAMDYWGQGT 17

DB 117 RYGNFYDWGQGT 130

RESULT 6

HV11_MOUSE
ID HV11_MOUSE STANDARD; PRT; 137 AA.

AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).

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DR EMBL; J00539; AAA38172.1; -.
DR PIR; A02038; G2MS43.
DR InterPro; IPR003006;
DR Pfam; PF00047; ig: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match 50.0%; Score 49; DB 1; Length 137;
Best Local Similarity 80.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 RAMDYWGQGT 17

DB 122 RYFDYWGQGT 131

RESULT 7

HV43_MOUSE
ID HV43_MOUSE STANDARD; PRT; 144 AA.

AC P01819;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 141 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Toneyawa S.;
RT "Two types of somatic recombination are necessary for the generation
RL of complete immunoglobulin heavy-chain genes.";
RL Nature 286:676-683(1980).
CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
CC DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
CC -----
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CC -----
DP EMBL; J00491; AAA38121.1; -
DR EMBL; V00768; CAA24149.1; -
DR PIR; A02094; G2MS14.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.
FT NON_TER 144 144
FT SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match 49.0%; Score 48; DB 1; Length 144;
Best Local Similarity 87.5%; Pred. No. 0.43;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 MDYWGQGT 17
Db 131 LDYWGQGT 138

RESULT 8
HV02_XENLA STANDARD; PRT; 135 AA.
AC P20957;
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION XIG14 PRECURSOR (FRAGMENT).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
RT from cDNA sequence: implications for evolution of immunoglobulin
RT domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC -----
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CC -----
DP EMBL; J03632; AAA49791.1; -
DR PIR; B31933; B31933.
DR InterPro; IPR003006; -.
```

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DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 18
FT CHAIN 19 135 IG HEAVY CHAIN V REGION XIG14.
FT NON_TER 135 135
SQ SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;

Query Match 48.5%; Score 47.5; DB 1; Length 135;
Best Local Similarity 69.2%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Qy 5 YNKRMDYWGQGT 17
Db 120 YN---FDYWGQGT 129

RESULT 9
HV35_MOUSE STANDARD; PRT; 111 AA.
AC P01804;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION HPC76 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=81013937; PubMed=6251474;
RA Bernard O., Gough N.M.;
RT "Nucleotide sequence of immunoglobulin heavy chain joining segments
RT between translocated VH and mu constant regions genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE FIRST 197 RESIDUES OF THE C
CC REGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM THE
CC CORRESPONDING PORTION OF THE MOUSE MOPC 104E MU CHAIN.
CC PIR; A02074; MHMS76.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region.
FT NON_TER 1 111
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12304 MW; 0EDE98EC7348056A CRC64;

Query Match 46.9%; Score 46; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DYWGQGT 17
Db 99 DYWGQGT 105

RESULT 10
HV3T_HUMAN STANDARD; PRT; 116 AA.
AC P01781;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN SEQUENCE.
RP MEDLINE=75059123; PubMed=4803843;
RX
```

RA Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
 RT "The primary structure of a monoclonal IgM-immunoglobulin
 (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
 type), subgroup H III. Architecture of the complete IgM-molecule.";
 RL Hoyer-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
 RN [2]
 RP REVISION TO THE COMPOSITION OF 28-33.
 RA Hilschmann N.;
 RL Submitted (JUN-1975) to the PIR data bank.
 CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN
 DR PIR: A02064; M3HUGL.
 DR HSP: P01772; 2IG2.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig: 1.
 KW Immunoglobulin V region.
 FT NON_TER 116
 SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match 46.9%; Score 46; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.74;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 DYWGQGT 17
 Db 104 DYWGQGT 110

RESULT 11
 ID HV39_MOUSE STANDARD; PRT; 118 AA.
 AC P01809;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION X24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79223895; PubMed=111245;
 RA Rao D.N., Rudikoff S., Kruttsch H., Potter M.;
 RT "Structural evidence for independent joining region gene in
 immunoglobulin heavy chains from anti-galactan myeloma proteins and
 its potential role in generating diversity in
 complementarity-determining regions.";
 RP Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
 CC THAT BINDS GALACTAN.
 DR PIR: A02079; AVMSX2.
 DR HSP: P01810; 2FBU.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig: 1.
 KW Immunoglobulin V region.
 FT NON_TER 118
 SQ SEQUENCE 118 AA; 13105 MW; BB16A2DB677EF17F CRC64;

Query Match 46.9%; Score 46; DB 1; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.75;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 DYWGQGT 17
 Db 105 DYWGQGT 111

RESULT 12
 ID HV03_MOUSE STANDARD; PRT; 120 AA.

AC P01747;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 36-65.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83131846; PubMed=6186498;
 RA Siekevitz M., Geffer M.L., Broder P., Riblet R.,
 RA Marshak-Rothstein A.;
 RT "The genetic basis of antibody production: the dominant anti-arsonate
 idiotype response of the strain A mouse.";
 RL Eur. J. Immunol. 12:1023-1032(1982).
 CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
 CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
 CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
 CC SEGMENT, JH2.
 DR PIR: A02028; HVMSG7.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig: 1.
 KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
 FT NON_TER 120
 SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 46.9%; Score 46; DB 1; Length 120;
 Best Local Similarity 100.0%; Pred. No. 0.76;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 DYWGQGT 17
 Db 108 DYWGQGT 114

RESULT 13
 ID HV1H_HUMAN STANDARD; PRT; 120 AA.
 AC P80421;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-I REGION DOT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95255298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig: 1.
 KW Immunoglobulin V region.
 FT DISULFID 22 95 BY SIMILARITY.
 FT NON_TER 120 120
 SQ SEQUENCE 120 AA; 13272 MW; F1307FD253A782F1 CRC64;

Query Match 46.9%; Score 46; DB 1; Length 120;
 Best Local Similarity 53.8%; Pred. No. 0.76;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 YNKRMDYWGQGT 17
 Db 102 FSQYGMVWGQGT 114


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RESULT 14
HV3K HUMAN
ID HV3K HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RI Opppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marquart M., Delsenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
RL J. Mol. Biol. 141:369-391(1980).
DR PIR; A02055; GIHUKL.
DR PDB; 2PB4; 12-JUL-89.
DR PDB; 2IG2; 12-JUL-89.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; 3D-structure.
FT MOD_RES 1 1
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 46 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 113
FT STRAND 120 124
FT NON_TER 126 126
SQ SEQUENCE 126 AA; E4D71B52B16F8776 CRC64;

Query Match 46.9%; Score 46; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DYWGQGT 17
| | | | |
Db 114 DYWGQGT 120

RESULT 15
HV46_MOUSE
ID HV46_MOUSE STANDARD; PRT; 137 AA.
AC P01822;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 315 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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CC -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
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CC EMBL; M27638; AAA61337.1; -.
CC EMBL; X07880; CAA30727.1; -.
DR PIR; PL0102; AVMS35.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 18
FT CHAIN 19 137
FT DOMAIN 19 48
FT COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 49 54
FT COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 55 68
FT DOMAIN 69 84
FT DOMAIN 85 116
FT DOMAIN 117 126
FT DOMAIN 127 137
FT DISULFID 40 114
FT CONFLICT 15 15
FT CONFLICT 15 15
IG HEAVY CHAIN V REGION MOPC 315.
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3.
FRAMEWORK 4.
BY SIMILARITY.
G -> GG (IN CAA30727).
G -> H (IN REF. 2).

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FT CONFLICT 77 78 GY -> YG (IN REF. 4).
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FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;

Query Match 46.9%; Score 46; DB 1; Length 137;
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QY 11 DYWGQGT 17
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Db 125 DYWGQGT 131

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